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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (ii) TITLE OF INVENTION: OB Protein Derivatives
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
- 10 (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 460 Point San Bruno Blvd
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
- 15 (F) ZIP: 94080
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 20 (D) SOFTWARE: WinPatin (Genentech)
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 19-Dec-1996
 - (C) CLASSIFICATION:
- 25 (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/667184
 - (B) FILING DATE: 20-JUN-1996
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/579494
- 30 (B) FILING DATE: 27-DEC-1995
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Dreger, Ginger R.
 - (B) REGISTRATION NUMBER: 33,055
 - (C) REFERENCE/DOCKET NUMBER: 985P2PCT
- 35 (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415/225-3216
 - (B) TELEFAX: 415/952-9881
 - (C) TELEX: 910/371-7168
 - (2) INFORMATION FOR SEQ ID NO:1:
- 40 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7127 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Double

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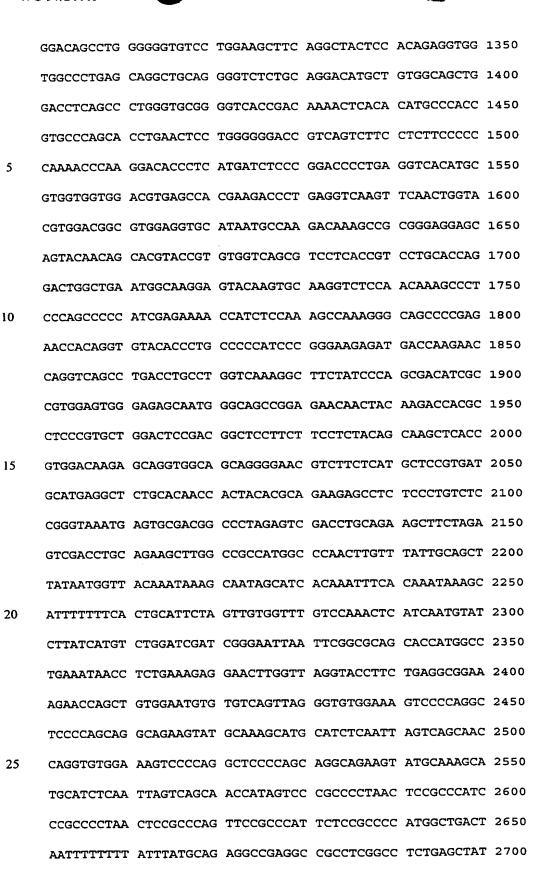
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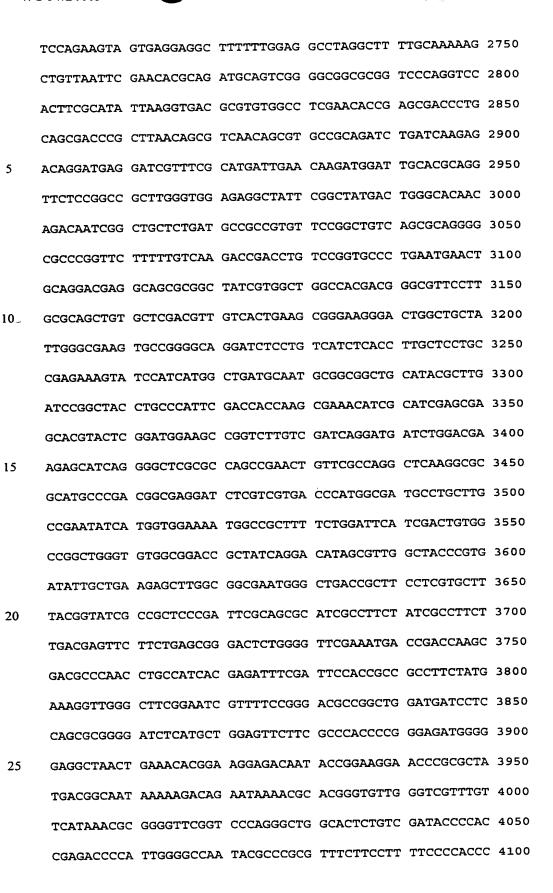
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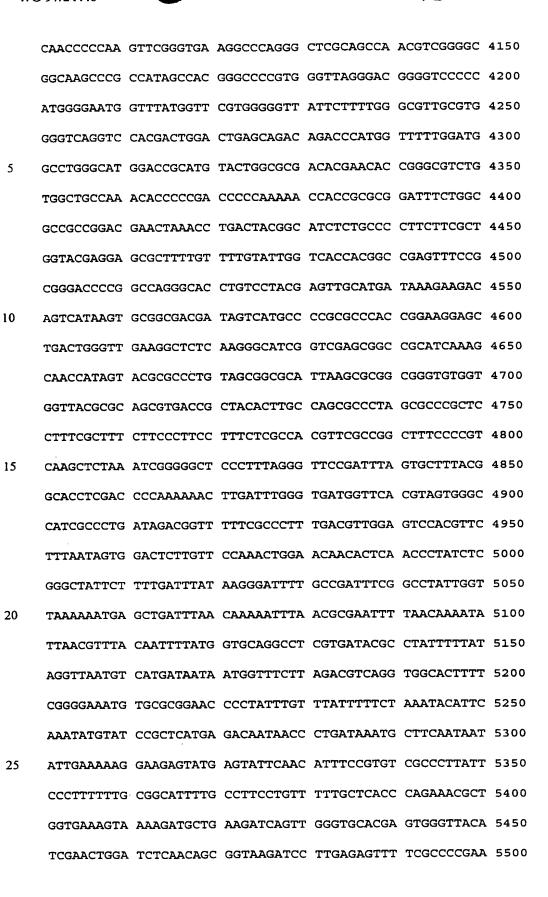
(D) TOPOLOGY: Linear

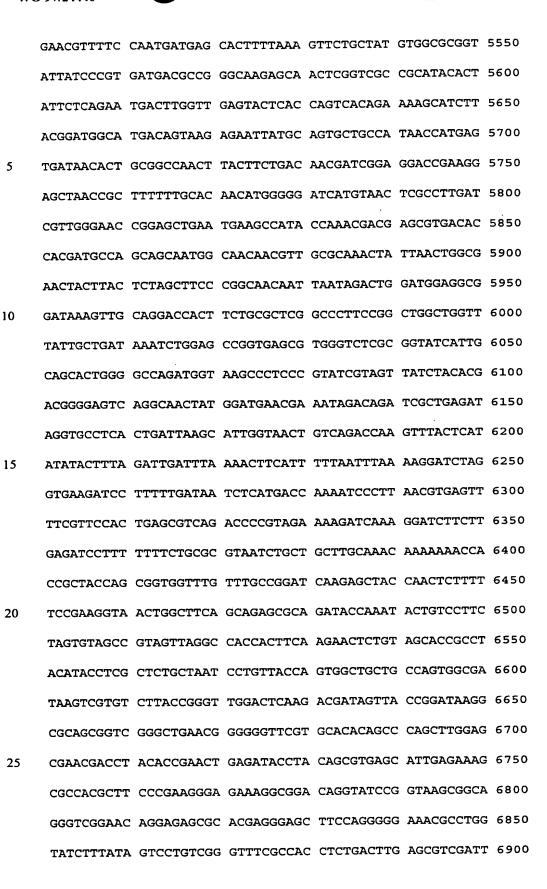
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTCGAGCTCG CCCGACATTG ATTATTGACT AGTTATTAAT AGTAATCAAT 50 TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC GTTACATAAC 100 TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG 150 ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA 200 TTGACGTCAA TGGGTGGAGT ATTTACGGTA AACTGCCCAC TTGGCAGTAC 250 ATCAAGTGTA TCATATGCCA AGTACGCCCC CTATTGACGT CAATGACGGT 300 AAATGGCCCG CCTGGCATTA TGCCCAGTAC ATGACCTTAT GGGACTTTCC 350 TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC 400 GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA 450 TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA 500 AAATCAACGG GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC 550 AAATGGGCGG TAGGCGTGTA CGGTGGGAGG TCTATATAAG CAGAGCTCGT 600 TTAGTGAACC GTCAGATCGC CTGGAGACGC CATCCACGCT GTTTTGACCT 650 CCATAGAAGA CACCGGGACC GATCCAGCCT CCGCGGCCGG GAACGGTGCA 700 TTGGAACGCG GATTCCCCGT GCCAAGAGTG ACGTAAGTAC CGCCTATAGA 750 GTCTATAGGC CCACCCCTT GGCTTCGTTA GAACGCGGCT ACAATTAATA 800 CATAACCTTA TGTATCATAC ACATACGATT TAGGTGACAC TATAGAATAA 850 CATCCACTTT GCCTTTCTCT CCACAGGTGT CCACTCCCAG GTCCAACTGC 900 ACCTCGGTTC TATCGATATG CATTGGGGAA CCCTGTGCGG ATTCTTGTGG 950 CTTTGGCCCT ATCTTTCTA TGTCCAAGCT GTGCCCATCC AAAAAGTCCA 1000 AGATGACACC AAAACCCTCA TCAAGACAAT TGTCACCAGG ATCAATGACA 1050 TTTCACACAC GCAGTCAGTC TCCTCCAAAC AGAAAGTCAC CGGTTTGGAC 1100 TTCATTCCTG GGCTCCACCC CATCCTGACC TTATCCAAGA TGGACCAGAC 1150 ACTGGCAGTC TACCAACAGA TCCTCACCAG TATGCCTTCC AGAAACGTGA 1200 TCCAAATATC CAACGACCTG GAGAACCTCC GGGATCTTCT TCACGTGCTG 1250 GCCTTCTCTA AGAGCTGCCA CTTGCCCTGG GCCAGTGGCC TGGAGACCTT 1300









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TTTGTGATGC TCGTCAGGGG GGCGGAGCCT ATGGAAAAAC GCCAGCTGGC 6950

ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT 7000

GTGAGTTACC TCACTCATTA GGCACCCCAG GCTTTACACT TTATGCTTCC 7050

GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA 7100

- 5 ACAGCTATGA CCATGATTAC GAATTAA 7127
 - (2) INFORMATION FOR SEQ ID NO:2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 397 amino acids
 - (B) TYPE: Amino Acid
- 10 (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	His	Trp	Gly	Thr	Leu	Cys	Gly	Phe	Leu	Trp	Leu	Trp	Pro	Tyr
1				5					10					15

Leu Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp
20 25 30

Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile
35 40 45

Ser His Thr Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu 50 55 60

20 Asp Phe Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met 65 70 75

Asp Gln Thr Leu Ala Val Tyr Gln Gln Ile Leu Thr Ser Met Pro 80 85 90

Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg 95 100 105

Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser Cys His Leu Pro 110 115 120

Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly Gly Val Leu 125 130 135

30 Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu 140 145 150

Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser Pro 155 160 165

Gly Cys Gly Val Thr Asp Lys Thr His Thr Cys Pro Pro Cys Pro 170 175 180

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro



PCT/US96/20

					185					190					195
	Lys	Pro	Lys	Asp	Thr 200	Leu	Met	Ile	Ser	Arg 205	Thr	Pro	Glu	Val	Thr 210
5	Cys	Val	Val	Val	Asp 215	Val	Ser	His	Glu	Asp 220	Pro	Glu	Val	Lys	Phe 225
	Asn	Trp	Tyr	Val	Asp 230	Gly	Val	Glu	Val	His 235	Asn	Ala	Lys	Thr	Lys 240
	Pro	Arg	Glu	Glu	Gln 245	Tyr	Asn	Ser	Thr	Tyr 250	Arg	Val	Val	Ser	Val 255
10	Leu	Thr	Val	Leu	His 260	Gln	Asp	Trp	Leu	Asn 265	Gly	Lys	Glu	Tyr	Lys 270
	Cys	Lys	Val	Ser	Asn 275	Lys	Ala	Leu	Pro	Ala 280	Pro	Ile	Glu	Lys	Thr 285
15	Ile	Ser	Lys	Ala	Lys 290	Gly	Gln	Pro	Arg	Glu 295	Pro	Gln	Val	Tyr	Thr 300
	Leu	Pro	Pro	Ser	Arg 305	Glu	Glu	Met	Thr	Lys 310	Asn	Gln	Val	Ser	Leu 315
	Thr	Cys	Leu	Val	Lys 320	Gly	Phe	Tyr	Pro	Ser 325	Asp	Ile	Ala	Val	Glu 330
20	Trp	Glu	Ser	Asn	Gly 335	Gln	Pro	Glu	Asn	Asn 340	Tyr	Lys	Thr	Thr	Pro 345
	Pro	Val	Leu	Asp	Ser 350	Asp	Gly	Ser	Phe	Phe 355	Leu	Tyr	Ser	Lys	Leu 360
25	Thr	Val	Asp	Lys	Ser 365		Trp	Gln	Gln	Gly 370		Val	Phe	Ser	Cys 375
	Ser	Val	. Met	His	Glu 380		Leu	His	Asn	His 385		Thr	Gln	Lys	Ser 390
	Leu	Ser	Leu	Ser	Pro 395		Lys 397								